REMARKS

Enclosed herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a Substitute Sequence Listing to be inserted into the specification as indicated above. The Substitute Sequence Listing in no way introduces new matter into the specification. Also submitted herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a disk copy of the Substitute Sequence Listing. The disk copy of the Sequence Listing, file "0020-4877P.ST25.txt", is identical to the paper copy, except that it lacks formatting.

The amendments to the Specification are being made to reference the sequences by their SEQ ID NOS. No new matter is introduced by these amendments.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,
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Attachments: Paper and Disk Copy of Sequence Listing, Copy of Notice

VERSION WITH MARKINGS TO SHOW CHANGES MADE

([Deleted material]shown in brackets, **added material** is shown in bold underline)

In the Specification:

Please replace the paragraph beginning on page 4, line 27, with the following rewritten paragraph:

--Fig. 1 shows the nucleotide sequence and predicted amino acid sequence of the cDNA coding human Fas protein (up to 284th amino acid). **(SEQ ID NO: 1)**--

Please replace the paragraph beginning on page 5, line 17, with the following rewritten paragraph:

--Fig. 8 shows the schematic representation of comparison in amino acid sequence of extracellular domain of the human Fas with other members of the NGFR/TNFR family. **(hFAS = SEQ ID NO: 3, hTNRF1 = SEQ ID NO: 4, hTNFR2 = SEQ ID NO: 5, hNGFR = SEQ ID NO: 6, hCD40 = SEQ ID NO: 7, rOX40 = SEQ ID NO: 8)**--

Please replace the paragraph beginning on page 5, line 20, with the following rewritten paragraph:

--Fig. 9 shows the comparative representation of the amino acid sequences of the cytoplasmic domains of the Fas **(SEQ ID NO: 10)**, TNF

receptor type I (**SEQ ID NO: 11**), and CD40 **(SEQ ID NO: 9)**.--

Please replace the paragraph beginning on page 17, line 12, with the following rewritten paragraph:

--With the current technical level in this field of science, it will be [esay] **easy** to introduce mutation such as deletions, additions, insertions and/or substitutions to the amino acid sequence without changing fundamental properties (e.g. physical properties, physiological or biological activity, immunological activity, etc.) of the proteins. For instance, substitution of a hydrophobic amino acid residue with other hydrophobic amino acid residue, or of amino acid residue having positive electric charge with other amino acid residue having positive electric charge, mutual substitution among Glu and Asp or Lys, His and Arg, substitution among Ile, Val, Met and Leu groups, substitution among Gly, Ala, Ser and Cys groups, and substitution among Trp, Tyr and Phe groups may be predicted. For easy purification of the protiens of the present invention, furthermore, other proteins such as [β-galactositase] **β-galactosidase** of [Eschaerichia coli] **Escherichia coli** or mouse IgG Fc fragment may be added to the N-terminal side or/and the C-terminal side of the proteins by the genetic engineering method, or the amino acid sequence may be partly cleaved or substituted by the similar method in order to more deeply analyze

the function of the proteins, as can easily be contrived by people skilled in the art. Therefore, such human Fas antigen amino acid mutants are also encompassed by the present invention. For instance, soluble Fas antigens indicated by amino acids Nos. 1 to 157**, as shown in Figure 1,** are preferred examples of such mutants.--